

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Wild, Hanno; Hanko, Rudolf; Dorschug, Michael; Horlein, Hans-Dietrich; Beunink, Jurgen; Apeler, Heiner; Wehlmann, Hermann; and Sebald, Walter

(ii) TITLE OF INVENTION: HIL-4 MUTANT PROTEINS USED AS ANTAGONISTS OR PARTIAL AGONISTS OF HUMAN INTERLEUKIN 4

(iii) NUMBER OF SEQUENCES: 5

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: Sprung Kramer Schaefer & Briscoe
(B) STREET: 660 White Plains Road
(C) CITY: Tarrytown
(D) STATE: New York
(E) COUNTRY: USA
(F) ZIP: 10591-5144

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage
(B) COMPUTER: Apple Macintosh
(C) OPERATING SYSTEM: System 7.5
(D) SOFTWARE: WordPerfect 3.5

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: 08/765,012
(B) FILING DATE: 19-DEC-1996
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: PCT/EP95/02358
- (B) FILING DATE: 19-JUN-1995

(viii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: DE 44 23 131
- (B) FILING DATE: 01-JUL-1994

(ix) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Kurt G. Briscoe
- (B) REGISTRATION NUMBER: 33,141
- (C) REFERENCE/DOCKET NUMBER: BAYER 9776-KGB

(x) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: (914) 332-1700
- (B) TELEFAX: (914) 332-1844

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: synthetic

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CATGCACAAG TGCGAT

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(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: synthetic

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

ATCGCACTTG TG

12

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: synthetic
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

GCCTCCAAGG ACACAACTGA G

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- (2) INFORMATION FOR SEQ ID NO: 4:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: synthetic
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

GTGAAGGAAG CCGACCAGAG TACG

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(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: synthetic

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

CTGGAGACTG CCATGGCCCA CAAGTGCGAT ATCACC

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